

## STIC Biotechnology Systems Branch

### RAW SEQUENCE LISTING ERROR REPORT

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: 10/525,326  
Source: PCT  
Date Processed by STIC: 3-4-05

**THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.**

**PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:**

- 1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,
- 2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY

**FOR CRF SUBMISSION AND PATENTIN SOFTWARE QUESTIONS, PLEASE CONTACT MARK SPENCER, TELEPHONE: 571-272-2510; FAX: 571-273-0221**

**TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE CHECKER VERSION 4.2.2 PROGRAM, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW FOR ADDRESS:**

**<http://www.uspto.gov/web/offices/pac/checker/chkrnote.htm>**

Applicants submitting genetic sequence information electronically on diskette or CD-Rom should be aware that there is a possibility that the disk/CD-Rom may have been affected by treatment given to all incoming mail. Please consider using alternate methods of submission for the disk/CD-Rom or replacement disk/CD-Rom. Any reply including a sequence listing in electronic form should NOT be sent to the 20231 zip code address for the United States Patent and Trademark Office, and instead should be sent via the following to the indicated addresses:

1. EFS-Bio (<http://www.uspto.gov/ebc/efs/downloads/documents.htm>) , EFS Submission User Manual - cPAVE)
2. U.S. Postal Service: Commissioner for Patents, P.O. Box 1450, Alexandria, VA 22313-1450
3. Hand Carry, Federal Express, United Parcel Service, or other delivery service (EFFECTIVE 01/14/05):  
U.S. Patent and Trademark Office, Mail Stop Sequence, Customer Window, Randolph Building, 401 Dulany Street, Alexandria, VA 22314

Revised 01/24/05



PCT

## RAW SEQUENCE LISTING

DATE: 03/04/2005

PATENT APPLICATION: US/10/525,326

TIME: 12:25:30

Input Set : A:\PTO.FG.txt

Output Set: N:\CRF4\03042005\J525326.raw

4 <110> APPLICANT: KYOWA HAKKO KOGYO CO., LTD  
 6 <120> TITLE OF INVENTION: An agent for prevention and/or treatment of asthma  
 8 <130> FILE REFERENCE: 11504WO1  
 C--> 10 <140> CURRENT APPLICATION NUMBER: US/10/525,326  
 C--> 11 <141> CURRENT FILING DATE: 2005-02-22  
 13 <150> PRIOR APPLICATION NUMBER: JP 2002/241523  
 14 <151> PRIOR FILING DATE: 2002-08-22  
 16 <160> NUMBER OF SEQ ID NOS: 18  
 18 <170> SOFTWARE: PatentIn Ver. 2.1

## ERRORED SEQUENCES

525 <210> SEQ ID NO: 15  
 526 <211> LENGTH: 36  
 527 <212> TYPE: DNA  
 528 <213> ORGANISM: Artificial Sequence  
 W--> 529 <220> FEATURE:  
 530 <223> OTHER INFORMATION: Description of Artificial Sequence: synthetic DNA  
 532 <400> SEQUENCE: 15  
 E--> 533 ataagcttgcacacatggacacacagcaggggcac  
 536 <210> SEQ ID NO: 16  
 537 <211> LENGTH: 33  
 538 <212> TYPE: DNA  
 539 <213> ORGANISM: Artificial Sequence  
 W--> 540 <220> FEATURE:  
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 624 <211> LENGTH: 1098  
 625 <212> TYPE: DNA  
 626 <213> ORGANISM: Rattus norvegicus  
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 630 Met Asp Asn Ser Thr Gly Thr Trp Glu Gly Cys His Val Asp Ser Arg  
 631 1 5 10 15  
 633 gtg gac cac ctc ttc cca cca tcc ctc tac atc ttc gtc atc ggg gtg 96  
 634 Val Asp His Leu Phe Pro Pro Ser Leu Tyr Ile Phe Val Ile Gly Val  
 635 20 25 30  
 637 ggg ctg ccc acc aac tgc ctg gcc ctg tgg gca gcc tac cgc cag gtg 144  
 638 Gly Leu Pro Thr Asn Cys Leu Ala Leu Trp Ala Ala Tyr Arg Gln Val  
 639 35 40 45

Does Not Comply  
 Corrected Diskette Needed  
 (pg. 1)

36-34

33-31

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Input Set : A:\PTO.FG.txt

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641	cgc	cag	cgc	aat	gag	ctg	ggc	gtc	tac	ctg	atg	aac	ttg	agc	atc	gca	192
642	Arg	Gln	Arg	Asn	Glu	Leu	Gly	Val	Tyr	Leu	Met	Asn	Leu	Ser	Ile	Ala	
643		50					55					60					
645	gac	ctg	ctg	tac	atc	tgt	acg	ctg	ccg	ctg	tgg	gtc	gac	tac	ttc	ctc	240
646	Asp	Leu	Leu	Tyr	Ile	Cys	Thr	Leu	Pro	Leu	Trp	Val	Asp	Tyr	Phe	Leu	
647	65					70					75				80		
649	cac	cat	gac	aac	tgg	atc	cac	ggc	ccc	ggc	tcc	tgc	aag	ctc	ttt	ggc	288
650	His	His	Asp	Asn	Trp	Ile	His	Gly	Pro	Gly	Ser	Cys	Lys	Leu	Phe	Gly	
651				85						90					95		
653	ttc	atc	ttc	tac	agc	aac	atc	tac	atc	agc	atc	gcc	ttc	ctg	tgc	tgc	336
654	Phe	Ile	Phe	Tyr	Ser	Asn	Ile	Tyr	Ile	Ser	Ile	Ala	Phe	Leu	Cys	Cys	
655				100						105				110			
657	atc	tcc	gtg	gac	cgc	tac	ctg	gct	gtg	gcc	cat	ccg	ctg	cgc	ttt	gcg	384
658	Ile	Ser	Val	Asp	Arg	Tyr	Leu	Ala	Val	Ala	His	Pro	Leu	Arg	Phe	Ala	
659			115					120					125				
661	cgc	ctg	cgc	cgg	gtc	aag	aca	gca	gta	gct	gtg	agc	tcc	gtg	gtc	tgg	432
662	Arg	Leu	Arg	Arg	Val	Lys	Thr	Ala	Val	Ala	Val	Ser	Ser	Val	Val	Trp	
663		130					135					140					
665	gcc	acc	gag	cta	ggc	gcc	aac	tgc	gca	ccg	ctc	ttt	cat	gac	gag	ctc	480
666	Ala	Thr	Glu	Leu	Gly	Ala	Asn	Ser	Ala	Pro	Leu	Phe	His	Asp	Glu	Leu	
667	145				150					155					160		
669	ttt	cgt	gat	cgc	tac	aac	cac	acc	ttc	tgc	ttc	gag	aag	ttc	ccc	atg	528
670	Phe	Arg	Asp	Arg	Tyr	Asn	His	Thr	Phe	Cys	Phe	Glu	Lys	Phe	Pro	Met	
671				165						170					175		
673	gag	cgc	tgg	gtg	gcc	tgg	atg	aac	ctg	tac	cgc	gtc	ttt	gtg	ggg	ttc	576
674	Glu	Arg	Trp	Val	Ala	Trp	Met	Asn	Leu	Tyr	Arg	Val	Phe	Val	Gly	Phe	
675			180					185						190			
677	ctc	ttc	ccc	tgg	gca	ctc	atg	ttg	ctg	tgc	tac	cgc	ggc	atc	ctg	cgg	624
678	Leu	Phe	Pro	Trp	Ala	Leu	Met	Leu	Leu	Cys	Tyr	Arg	Gly	Ile	Leu	Arg	
679			195					200					205				
681	gcc	gta	cag	agc	agt	gtg	tcc	acc	gag	cgc	cag	gag	aaa	gtc	aag	atc	672
682	Ala	Val	Gln	Ser	Ser	Val	Thr	Glu	Arg	Gln	Glu	Lys	Val	Lys	Ile		
683		210					215					220					
685	aaa	cgc	ctg	gcc	ctg	agc	ctc	atc	gcc	atc	gtg	ctg	gtg	tgc	ttt	gca	720
686	Lys	Arg	Leu	Ala	Leu	Ser	Leu	Ile	Ala	Ile	Val	Leu	Val	Cys	Phe	Ala	
687	225				230					235					240		
689	ccc	tac	cat	gct	ctc	ttg	ctg	tct	cgc	agc	gct	gtc	tat	ctg	ggc	cgg	768
690	Pro	Tyr	His	Ala	Leu	Leu	Leu	Ser	Arg	Ser	Ala	Val	Tyr	Leu	Gly	Arg	
691				245						250					255		
693	ccc	tgg	gac	tgt	ggc	ttc	gag	gag	cga	gtc	ttc	tct	gcc	tac	cac	agc	816
694	Pro	Trp	Asp	Cys	Gly	Phe	Glu	Glu	Arg	Val	Phe	Ser	Ala	Tyr	His	Ser	
695			260						265					270			
697	tcc	cta	gcc	ttc	acc	agc	ctc	aat	tgc	gtg	gct	gac	ccc	atc	ctc	tac	864
698	Ser	Leu	Ala	Phe	Thr	Ser	Leu	Asn	Cys	Val	Ala	Asp	Pro	Ile	Leu	Tyr	
699			275					280						285			
701	tgc	ctg	gtc	aac	gag	ggt	gcc	cgt	agt	gac	gtg	gcc	aaa	gcc	ctg	cac	912
702	Cys	Leu	Val	Asn	Glu	Gly	Ala	Arg	Ser	Asp	Val	Ala	Lys	Ala	Leu	His	
703		290					295					300					
705	aac	ctc	ctc	cgc	ttc	ctg	gcc	agc	aac	aag	ccc	cag	gag	atg	gcc	aat	960

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```
706 Asn Leu Leu Arg Phe Leu Ala Ser Asn Lys Pro Gln Glu Met Ala Asn
707 305                      310                      315                      320
709 gct tcc ctc acc ctg gag aca cca ttg acc tcc aag agg agc acc acc      1008
710 Ala Ser Leu Thr Leu Glu Thr Pro Leu Thr Ser Lys Arg Ser Thr Thr
711                      325                      330                      335
713 ggc aaa acg tct ggg gct gtc tgg gca gtg cct ccc act gcc cag ggg      1056
714 Gly Lys Thr Ser Gly Ala Val Trp Ala Val Pro Pro Thr Ala Gln Gly
715                      340                      345                      350
717 gac cag gtg cca ctg aag gtg ctg ctg ccc ccg gca cag tga      1098
718 Asp Gln Val Pro Leu Lys Val Leu Leu Pro Pro Ala Gln
719                      355                      360                      365
```

E--&gt;

725 1/21

*pls delete*

## VERIFICATION SUMMARY

PATENT APPLICATION: US/10/525,326

DATE: 03/04/2005

TIME: 12:25:31

Input Set : A:\PTO.FG.txt

Output Set: N:\CRF4\03042005\J525326.raw

L:10 M:270 C: Current Application Number differs, Replaced Application Number  
L:11 M:271 C: Current Filing Date differs, Replaced Current Filing Date  
L:529 M:283 W: Missing Blank Line separator, <220> field identifier  
L:533 M:254 E: No. of Bases conflict, LENGTH:Input:36 Counted:34 SEQ:15  
L:533 M:252 E: No. of Seq. differs, <211> LENGTH:Input:36 Found:34 SEQ:15  
L:540 M:283 W: Missing Blank Line separator, <220> field identifier  
L:544 M:254 E: No. of Bases conflict, LENGTH:Input:33 Counted:31 SEQ:16  
L:544 M:252 E: No. of Seq. differs, <211> LENGTH:Input:33 Found:31 SEQ:16 ✓  
L:725 M:254 E: No. of Bases conflict, LENGTH:Input:21 Counted:1099 SEQ:18 ✓  
L:725 M:320 E: (1) Wrong Nucleic Acid Designator, NUMBER OF INVALID KEYS:2 ✓  
L:725 M:252 E: No. of Seq. differs, <211> LENGTH:Input:1098 Found:1099 SEQ:18 ✓